ASSOCIATION BETWEEN *IL10R1* S138G LOSS-OF-FUNCTION POLYMORPHISM WITH EXTRAPULMONARY TUBERCULOSIS IN TUNISIA

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Introduction:

Tuberculosis (TB) remains the single infectious disease, causing the highest mortality in humans, leading to 1,3 million deaths annually. IL10 cytokine exerts a variety of immunorulatory activities, which affect both of innate and cell-mediated immunity through its cellular receptor (IL10R1). Given its key role in the control of TB, we have investigated possible association between *IL10R1* S138G loss-of-function polymorphism and risk development of active TB in Tunisia.

Materials and methods:

Genomic DNA samples were obtained from 223 patients with active TB (168 pulmonary and 55 extrapulmonary cases) and 150 healthy blood donors. Genotypes were analyzed using allele-specific PCR.

Results:

The G allele [odds ratio OR= 5.01; P= 10^{-7}], GG genotypes [OR=9.06; correcting P-values using the Bonferroni method for multiple tests Pc= 0.015] and AG genotype [OR= 3.75; 95% CI (1.62–8.7); Pc= 0.0012] seemed to be associated with the risk development of active extrapulmonary TB were found. In contrast, the AA genotype seemed to be associated with resistance to extrapulmonary tuberculosis [OR= 0.19; 95% CI (0.09–0.42); Pc= 6.10^{-6}]. No association was found between S138G polymorphism and pulmonary TB.

S138G allele and genotype frequencies (n, %) in extrapulmonary tuberculosis cases and controls.

[d]: The AA genotype served as reference category, CC or AC versus AA

	epTB (N=55) (%)	Controls (N=150) (%)	P	OR
Allele				
C	29 (26)	20 (7)	10^{-7}	5.01
A	81 (74)	280 (93)		
Genotype				
CC	6 (11)	2 (1)	0.005* (0.015)	9.06
AC	17 (31)	16 (11)	0.0004 (0.0012)	3.75
AA[d]	32 (58)	132 (88)	2.10^{-6} (6.10^{-6})	0.19

Conclusion:

Our study suggested that the *IL-10R1* S138G loss-of-function polymorphism may contribute to susceptibility to extrapulmonary TB in Tunisian populations.